

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bartsch, Dusan  
Kandel, Eric R.  
Ghirardi, Mirella
- (ii) TITLE OF INVENTION: A METHOD FOR ENHANCING LONG-TERM MEMORY  
IN A SUBJECT AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Cooper & Dunham LLP
  - (B) STREET: 1185 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: White, John P.
  - (B) REGISTRATION NUMBER: 28,678
  - (C) REFERENCE/DOCKET NUMBER: 50865/JPW/JML
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 212-278-0400
  - (B) TELEFAX: 212-391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Leu	Asp	Leu	Trp	Ser	Glu	Asp	Phe	Gln	Leu	Ala	Arg	Glu	Trp
1				5					10					15	
Gly	Leu	Glu	Met	Pro	Val	Val	Gln	Thr	Asp	Gly	Gln	Phe	Gly	Asp	Leu
			20					25					30		
Lys	Ser	Thr	Ser	Arg	His	Gly	Gly	Asp	Glu	Ser	Leu	Ser	Leu	Gln	Pro
		35					40					45			
Gln	Gly	Ala	Thr	Leu	Lys	Leu	Glu	Pro	Phe	Glu	Glu	Asp	Val	Leu	Gly
	50					55					60				
Ala	Glu	Trp	Met	Glu	Ser	Ser	Asp	Leu	Gly	Ser	Phe	Leu	Asp	Ala	Leu
65					70					75					80
Gly	Asp	Asn	His	Glu	Arg	Leu	His	Pro	Phe	Glu	Ser	Asn	Leu	Leu	Glu
				85					90					95	
Phe	Thr	Ser	Leu	Ile	Thr	Pro	Asp	Asp	Ser	Thr	Val	Ser	Lys	Asp	Ile
			100					105					110		
Leu	Ser	Ser	Thr	Leu	Gln	Phe	Pro	Thr	Gln	Pro	Val	Asn	Ile	Pro	Leu
		115					120					125			
Tyr	Ala	Ser	His	Gly	Ala	Glu	Asp	Phe	Ser	Ala	Glu	Thr	Glu	Phe	Glu
	130					135					140				
Asn	His	Leu	Ser	Pro	Pro	Asp	Ser	Pro	Glu	Gln	Val	Ala	Pro	Val	Ile
145					150					155					160
Asn	Leu	Glu	Pro	Val	Glu	Leu	Thr	Ala	Ser	His	Met	Thr	Val	Ile	Ser
				165					170					175	
Pro	Asp	Gly	Leu	Leu	Gly	Gly	Met	Glu	Leu	Ala	Ser	Glu	Ser	Leu	Thr
			180					185					190		
Phe	Thr	Glu	Leu	Asp	Phe	Val	Asn	Phe	Asn	Asp	Ser	Ala	Val	Gly	Ser
		195					200					205			
Ile	Gly	Gly	Ala	Glu	Glu	Leu	Leu	Gly	Ser	Pro	Leu	Ser	Val	Asp	Asp
	210					215					220				
Val	Glu	Ser	Thr	Ile	Ser	Phe	Ser	Gly	Pro	Ser	Ser	Pro	Glu	Thr	Ser
225					230					235					240
Gln	Ser	Ser	Ile	Ile	Glu	Ser	Ser	Pro	Glu	Leu	Tyr	Lys	Val	Ile	Ser
				245					250					255	

Thr	Ser	Ser	Ile	Asp	Ala	Ser	Lys	Arg	Phe	Ser	Pro	Tyr	Ser	Arg	Ser			
			260					265					270					
Ser	Lys	Ser	Lys	Gln	Ser	Val	Lys	Thr	Ser	Asp	Ala	Lys	Ala	Pro	Arg			
			275				280					285						
Lys	Thr	Arg	Thr	Pro	Ala	Gln	Pro	Val	Pro	Glu	His	Val	Ile	Met	Glu			
			290			295					300							
His	Leu	Asp	Lys	Lys	Asp	Arg	Lys	Lys	Leu	Gln	Asn	Lys	Asn	Ala	Ala			
305					310					315					320			
Ile	Arg	Tyr	Arg	Met	Lys	Lys	Lys	Gly	Glu	Ala	Gln	Gly	Ile	Lys	Gly			
				325					330					335				
Glu	Glu	Gln	Glu	Leu	Glu	Glu	Leu	Asn	Thr	Lys	Leu	Lys	Thr	Lys	Val			
			340					345					350					
Asp	Asp	Leu	Gln	Arg	Glu	Ile	Lys	Tyr	Met	Lys	Asn	Leu	Met	Glu	Asp			
		355					360					365						
Val	Cys	Lys	Ala	Lys	Gly	Ile	Gln	Leu	Lys	Met								
		370				375												

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu	Asp	Lys	Lys	Asp	Arg	Lys	Lys	Leu	Gln	Asn	Lys	Asn	Ala	Ala	Ile			
1				5				10					15					
Arg	Tyr	Arg	Met	Lys	Lys	Lys	Gly	Glu	Ala	Gln	Gly	Ile	Lys	Gly	Glu			
			20				25					30						
Glu	Gln	Glu	Leu	Glu	Glu	Leu	Asn	Thr	Lys	Leu	Lys	Thr	Lys	Val	Asp			
		35				40						45						
Asp	Leu	Gln	Arg	Glu	Ile	Lys	Tyr	Met	Lys	Asn	Leu	Met	Glu	Asp	Val			
		50				55					60							

Cys Lys Ala Lys Gly Ile Gln Leu Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGACGTCA

8

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGTATTGCGT CATC

14

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTATTGCGC AATC

14

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCCGCTTTC CATAAGTCGA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACCTGAAAAT GATATTGTAC

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCCGGCGC CTCCTTGGCT GACGTCAGAG AGAGAGA

37

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCCGGCTG ACGTCATCAA GCTA

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCCCCTTA CGTCAGAGGC GA

22

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCCGGCGC GGGGCTGGCG TAGGGCCTGC GTCAGCTGCA

40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTGGCATC TACGTCAAGG CTTC

24

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCCGGCAG TATTGCGTCA TCTCAAGCTA

30

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATCCGGCTG ACGCAATTCA AGCTA

25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCCACAGT TGTGATTTC A AACCTGACC AGA

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCCGGCAC TATTGCGCAA TCTCAAGCTA

30

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCCATATT AAGGACATGC CG

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1336 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACGCTACAGA	ACGGTCAAGA	AATATAATGT	GTGCAAAGAT	GTCTGCTTAG	GAAGACACGG	60
CGACGTCCGC	CCCCAAGGGC	AATCGGCACA	ATGGCAACCT	TTCATGATGT	ATTCCTAGCT	120
ACGGCTATCT	CGCTTCTCTA	TTGGACGGAT	TTATTTATCA	CATAGAAGAC	TCGTATACCA	180
AACTCTACGA	TGGAGCTGGA	CCTTTGGAGC	GAAGATTTTC	AACTGGCCAG	GGAATGGGGG	240
CTGGAAATGC	CAGTCGTCCA	GACCGATGGC	CAGTTCGGTG	ACCTCAAATC	AACCAGTCGT	300
CATGGTGGCG	ACGAATCTCT	AAGTTTGCAG	CCCCAGGGCG	CTACACTGAA	GTTGGAACCC	360
TTTGAGGAAG	ATGTCCTTGG	TGCAGAGTGG	ATGGAGTCGT	CCGATCTCGG	CTCTTTTCTG	420
GATGCTTTGG	GTGACAACCA	TGAGCGGCTG	CATCCGTTCT	AGTCAAACCT	GCTCGAGTTC	480
ACTTCTCTGA	TCACTCCTGA	TGATTCGACG	GTGTCAAAGG	ACATTCTCAG	CTCAACTCTT	540
CAGTTTCCAA	CTCAACCAGT	GAACATCCCT	TTATATGCAA	GTCATGGGGC	CGAAGATTTT	600
TCTGCAGAGA	CTGAGTTTGA	GAACCACCTG	TCGCCTCCAG	ATTCTCCGGA	GCAGGTAGCC	660
CCTGTCATAA	ATCTAGAACC	AGTTGAACTC	ACTGCGAGCC	ATATGACGGT	GATCTCACCT	720
GATGGCTTGT	TGGGTGGCAT	GGAAC TGGCT	TCAGAAAGCT	TAACATTTAC	CGAACTAGAC	780
TTTGTGAACT	TCAATGACAG	TGCTGTTGGT	TCAATTGGCG	GTGCTGAAGA	ACTTCTTGGC	840
TCCCCACTGT	CAGTTGATGA	TGTGGAAAGT	ACAATATCAT	TTTCAGGTCC	ATCGTCGCCA	900
GAAACCAGCC	AGAGCAGCAT	CATTGAATCA	AGTCCTGAAT	TGTACAAAGT	TATCTCTACC	960
TCGTCCATTG	ATGCATCTAA	GCGTTTCTCT	CCATACTCTC	GTTCTCTCAA	GTCCAAGCAA	1020
TCTGTCAAGA	CTTCAGACGC	TAAGGCACCT	CGTAAAACGA	GGACACCGGC	GCAGCCTGTG	1080
CCAGAACATG	TCATCATGGA	ACATTTGGAC	AAAAAGGACA	GAAAGAAGCT	TCAGAACAAG	1140
AATGCTGCCA	TTAGGTATAG	GATGAAGAAG	AAGGGGGAGG	CTCAGGGCAT	CAAAGGGGAG	1200
GAACAGGAAT	TAGAAGAACT	CAACACAAAG	CTTAAGACTA	AGGTCGATGA	CTTGCAAAGA	1260

GAAATCAAGT ACATGAAAAA TTTAATGGAA GATGTTTGCA AGGCGAAAAG TATTCAGCTT 1320  
AAATAGTGGG AAGGGT 1336

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu	Asp	Lys	Lys	Leu	Lys	Lys	Met	Glu	Gln	Asn	Lys	Thr	Ala	Ala	Thr
1				5					10					15	
Arg	Tyr	Arg	Gln	Lys	Lys	Arg	Ala	Glu	Gln	Glu	Ala	Leu	Thr	Gly	Glu
			20					25					30		
Cys	Lys	Glu	Leu	Glu	Lys	Lys	Asn	Glu	Ala	Leu	Lys	Glu	Lys	Ala	Asp
		35					40					45			
Ser	Leu	Ala	Lys	Glu	Ile	Gln	Tyr	Leu	Lys	Asp	Leu	Ile	Glu	Glu	Val
	50					55					60				
Arg	Lys	Ala	Arg	Gly	Lys	Lys	Arg	Val	Pro						
	65					70									

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu	Asp	Lys	Lys	Leu	Lys	Lys	Met	Glu	Gln	Asn	Lys	Thr	Ala	Ala	Thr
1				5					10					15	

-75-

Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu Ala Leu Thr Gly Glu  
20 25 30

Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu Lys Glu Arg Ala Asp  
35 40 45

Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp Leu Ile Glu Glu Val  
50 55 60

Arg Lys Ala Arg Gly Lys Lys Arg Val Pro  
65 70